

4

096,004 - SeqList.ST25.txt
SEQUENCE LISTING



<110> Geron Corporation
McWhir, Jim
Gold, Joseph D.
Schiff, J. Michael

<120> 096,004 - SeqList

<130> 096,004 - SeqList

<140> 09/995,149

<141> 2001-11-26

<150> 60/253,357

<151> 2000-11-27

<160> 20

<170> PatentIn version 3.1

<210> 1

<211> 15418

<212> DNA

<213> Homo sapiens

<400> 1

gcggccgcga gctctaatac gactcactat agggcgctcga ctcgatcaat ggaagatgag	60
gcattgccga agaaaagatt aatggatttg aacacacagc aacagaaact acatgaagtg	120
aaacacagga aaaaaaagat aaagaaacga aaagaaaagg gcatcagtga gcttcagcag	180
aagttccatc ggccttacat atgtgtaagc agaggccctg taggagcaga ggcaggggga	240
aaatacttta agaaataatg tctaaaagtt tttcaaatac gaggaaaaac ataaaaccac	300
agatccaaga agctcaacaa aacaaaagcac aagaaacagg aagaaattaa aagttatatc	360
acagtcaaat tgctgaaaac cagcaacaaa gagaatatct taagagtatc agaggaaaag	420
agattaatga caggccaaga aacaatgaaa acaatacaga tttcttgtag gaaacacaag	480
acaaaagaca ttttttaaaa ccaaaaaggaa aaaaaatgct acattaaaaat gttttttacc	540
cactgaaagt atatttcaaa acatatttta ggccaggcctt ggtggctcac acctgtaatc	600
ccagcacttt gggaggccaa ggtgggtgga tcgcttaagg tcaggagttc gagaccagcc	660
tgccaatat agcgaaaacc catctgtact aaaaacacaa aaattagctg ggtgtggtga	720
cacatgcctg taatcccagg tactcaggag gctaaggcag gagaattgct tgaactggga	780
ggcagagggtg gtgagccaag attgcaccag tgcactccag ccttgggtgac agagtgaac	840
tccatctcaa aaacaaacaa acaaaaatata tatacataaa tatatatgca catatatata	900
catatatataa tatatatata catatatataa tctatatata tatatacata tatacacata	960
tataaatcta tatacatata tatacatata taatatattt acatatataa atatatacat	1020
atataaatat acatatataa atacatatat aaatatacat atataaatat acatatataa	1080

096,004 - SeqList.ST25.txt

atatacatat ataaatatat acatatataa atatacatat ataaatatat atacatatat	1140
aaatatataa atatacaagt atatacaaat atatacatat ataaatgtat atacgtatat	1200
acatatatat ataaatatat aaaaaaactt ttggctgggc acctttccaa atctcatggc	1260
acataaagt ctcatggtaa cctcaaataa aaaaacatat aacagataca ccaaaaaataa	1320
aaaccaataa attaaatcat gccaccagaa gaaattacct tcactaaaag gaacacagga	1380
aggaaagaaa gaaggaagag aagaccatga aacaaccaga aaacaaacaa caaaacagca	1440
ggagtaattc ctgacttatc aataataatg ctgggtgtaa atggactaaa ctctccaatc	1500
aaaagacata gagggtgta atggacgaaa aaaacaagac tcaataatct gttgcctaca	1560
agaatatact tcacctataa agggacacat agactgaaaa taaaaggaag gaaaaatatt	1620
ctatgcaaat ggaaaccaa aaaagaacag aactagctac acttatatca gacaaaatag	1680
atttcaagac aaaaagtaca aaaagagaca aagtaattat ataataataa agcaaaaaaga	1740
tataacaatt gtgaatttat atgcgcccac cactgggaca cccagatata tacagcaaat	1800
attattagaa ctaaggagag agagagatcc ccatacaata atagctggag acttcacccc	1860
gcttttagca ttggacagat catccagaca gaaaatcaac caaaaaattg gacttaatct	1920
ataatataga acaaatgtac ctaattgatg tttacaagac atttcatcca gtagttgcag	1980
aatatgcatt ttttcctcag catatggatc atttcaagg atagaccata tattaggcca	2040
cagaacaagc cattaaaaat tcaaaaaaat tgagccaggc atgatggctt atgcttgtaa	2100
ttacagcact ttggggaggg tgaggtggga ggatgtcttg agtacaggag tttagacca	2160
gcctgggcaa aatagtgaga ccctgtctct acaaaacttt ttttttaatt agccaggcat	2220
agtggtgtgt gcctgtagtc ccagctactt aggaggctga agtggggagga tcacttgagc	2280
ccaagagttc aaggctacgg tgagccatga ttgcaacacc acacaccagc cttggtgaca	2340
gaatgagacc ctgtctcaaa aaaaaaaaaa aaaattgaaa taatataaag catcttctct	2400
ggccacagtg gaacaaaacc agaaatcaac aacaagagga attttgaaaa ctatacaaac	2460
acatgaaaat taaacaatat acttctgaat aaccagtgag tcaatgaaga aattaaaaag	2520
gaaattgaaa aatttatitta agcaaatgat aacggaaaca taacctctca aaaccacgg	2580
tatacagcaa aagcagtgct aagaaggaag tttatagcta taagcagcta catcaaaaaa	2640
gtagaaaagc caggcgagc ggctcatgcc tgtaatccca gcactttggg aggccaaggc	2700
gggcagatcg cctgaggcca ggagttcgag accagcctga ccaacacaga gaaaccttgt	2760
cgctactaaa aatacaaaat tagctgggca tggtggcaca tgcctgtaat cccagctact	2820
cgggaggctg aggcaggata accgcttgaa cccaggagggt ggaggttgcg gtgagccggg	2880
attgcgccat tggactccag cctgggtaac aagagtgaaa ccctgtctca agaaaaaaaa	2940
aaaagtagaa aaacttaaaa atacaaccta atgatgcacc ttaaagaact agaaaagcaa	3000

096,004 - SeqList.ST25.txt

gagcaaaacta	aacctaataat	tggtaaaaga	aaagaaataa	taaagatcag	agcagaaata	3060
aatgaaactg	aaagataaca	atacaaaaaga	tcaacaaaat	taaaagttgg	ttttttgaaa	3120
agataaaca	aattgacaaa	cctttgcccc	gactaagaaa	aaaggaaaaga	agacctaata	3180
aaataaagtc	agagatgaaa	aaagagacat	tacaactgat	accacagaaa	ttcaaaggat	3240
cactagaggc	tactatgagc	aactgtacac	taataaattg	aaaaacctag	aaaaaataga	3300
taaattccta	gatgcataca	acctaccaag	attgaaccat	gaagaaatcc	aaagcccaaa	3360
cagaccaata	acaataatgg	gattaaagcc	ataataaaaa	gtctcctagc	aaagagaagc	3420
ccaggaccca	atggcttccc	tgctggattt	taccaatcat	ttaaagaaga	atgaattcca	3480
atcctactca	aactattctg	aaaaatagag	gaaagaatac	ttccaaactc	attctacatg	3540
gccagtatta	ccctgattcc	aaaaccagac	aaaaacacat	caaaaacaaa	caaacaaaaa	3600
aacagaaaaga	aagaaaacta	caggccaata	tccctgatga	atactgatac	aaaaatcctc	3660
aacaaaacac	tagcaaacca	aattaaaca	caccttcgaa	agatcattca	ttgtgatcaa	3720
gtgggattta	ttccagggat	ggaaggatgg	ttcaacatat	gcaaatcaat	caatgtgata	3780
catcatccca	acaaaatgaa	gtacaaaaac	tatatgatta	tttacttta	tgagaaaaa	3840
gcatttgata	aaattctgca	cccttcatga	taaaaaccct	caaaaaacca	ggtatacaag	3900
aaacatacag	gccaggcaca	gtggctcaca	cctgcgatcc	cagcactctg	ggaggccaag	3960
gtgggatgat	tgcttggggc	caggagtttg	agactagcct	gggcaacaaa	atgagacctg	4020
gtctacaaaa	aactttttta	aaaaattagc	caggcatgat	ggcatatgcc	tgtagtccca	4080
gctagtctgg	aggctgaggt	gggagaatca	cttaagccta	ggaggctcag	gctgcagtga	4140
gccatgaaca	tgctactgta	ctccagccta	gacaacagaa	caagacccca	ctgaataaga	4200
agaaggagaa	ggagaaggga	gaaaggaggg	agaaggagg	aggaggagaa	ggaggaggtg	4260
gaggagaagt	ggaaggggaa	ggggaaggga	aagaggaaga	agaagaaaca	tatttcaaca	4320
taataaaagc	cctatatgac	agaccgaggt	agtattatga	ggaaaaactg	aaagcctttc	4380
ctctaagatc	tggaaaatga	caagggccca	ctttcaccac	tgtgattcaa	catagtacta	4440
gaagtcctag	ctagagcaat	cagataagag	aaagaaataa	aaggcatcca	aactggaaaag	4500
gaagaagtca	aattatcctg	tttgcatg	atatgatctt	atatctggaa	aagacttaag	4560
acaccactaa	aaaactatta	gagctgaaat	ttggtacagc	aggatacaaa	atcaatgtac	4620
aaaaatcagt	agtattttcta	tattccaaca	gcaaacatc	tgaaaaagaa	accaaaaaag	4680
cagctacaaa	taaaattaaa	cagctaggaa	ttaaccaaag	aagtgaagaa	tctctacaat	4740
gaaaactata	aaatattgat	aaaagaaatt	gaagagggca	caaaaaaaga	aaagatatct	4800
catgttcata	gattggaaga	ataaatactg	ttaaaatgtc	catactaccc	aaagcaattt	4860

096,004 - SeqList.ST25.txt

acaaattcaa	tgcaatccct	attaaaaatac	taatgacgtt	cttcacagaa	atagaagaaa	4920
caatttctaag	atttgtacag	aaccacaaaa	gaccagaat	agccaaagct	atcctgacca	4980
aaaagaacaa	aactggaagc	atcacattac	ctgacttcaa	attatactac	aaagctatag	5040
taacccaaac	tacatggtac	tggcataaaa	acagatgaga	catggaccag	aggaacagaa	5100
tagagaatcc	agaaacaaat	ccatgcatct	acagtgaact	cattttttgac	aaaggtgcca	5160
agaacatact	ttgggggaaa	gataatctct	tcaataaatg	gtgctggagg	aactggatat	5220
ccatatgcaa	aataacaata	ctagaactct	gtctctcacc	atatacaaaa	gcaaatcaaa	5280
atggatgaaa	ggcttaaadc	taaaacctca	aacttttgcaa	ctactaaaag	aaaacaccgg	5340
agaaactctc	caggacattg	gagtgggcaa	agacttcttg	agtaattccc	tgcaggcaca	5400
ggcaaccaa	gcaaaaacag	acaaatggga	tcatatcaag	ttaaaaagct	tctgcccagc	5460
aaaggaaaca	atcaacaaaag	agaagagaca	acccacagaa	tgggagaata	tatttgcaaa	5520
ctattcatct	aacaaggaat	taataaccag	tatatataag	gagctcaaac	tactctataa	5580
gaaaaacacc	taataagctg	attttcaaaa	ataagcaaaa	gatctgggta	gacatttctc	5640
aaaataagtc	atacaaatgg	caaacaggca	tctgaaaatg	tgctcaacac	caactgatcat	5700
cagagaaatg	caaatcaaaa	ctactatgag	agatcatctc	accccagtta	aaatggcttt	5760
tattcaaaaag	acaggcaata	acaaatgcca	gtgaggatgt	ggataaaaagg	aaacccttgg	5820
acactgtttg	tgggaatgga	aattgctacc	actatggaga	acagtttgaa	agttcctcaa	5880
aaaactaaaa	ataaagctac	catacagcaa	tcccattgct	aggtatatac	tccaaaaaag	5940
ggaatcagtg	tatcaacaag	ctatctccac	tcccacattt	actgcagcac	tgttcatagc	6000
agccaagggt	tggaagcaac	ctcagtgtcc	atcaacagac	gaatggaaaa	agaaaatgtg	6060
gtgcacatac	acaatggagt	actacgcagc	cataaaaaag	aatgagatcc	tgctcagttgc	6120
aacagcatgg	ggggcactgg	tcagtatgtt	aagtgaata	agccaggcac	agaaagacaa	6180
acttttcatg	ttctccccta	cttgtgggag	caaaaattaa	aacaattgac	atagaaatag	6240
aggagaatgg	tggttctaga	ggggtggggg	acagggtgac	tagagtcaac	aataatttat	6300
tgtatgtttt	aaaataacta	aaagagtata	attgggttgt	ttgtaacaca	aagaaaggat	6360
aaatgcttga	aggtagacaga	taccccatth	accctgatgt	gattattaca	cattgtatgc	6420
ctgtatcaaa	atatctcatg	tatgctatag	atataaaccc	tactatatta	aaaattaaaa	6480
ttttaatggc	caggcacggt	ggctcatgtc	cataatccca	gcactttggg	aggccgaggc	6540
ggtggatcac	ctgagggtcag	gagtttgaaa	ccagtctggc	caccatgatg	aaaccctgtc	6600
tctactaaaag	atacaaaaat	tagccaggcg	tggtggcaca	tacctgtagt	cccaactact	6660
caggaggctg	agacaggaga	attgcttgaa	cctgggaggc	ggagggttga	gtgagccgag	6720
atcatgccac	tgcactgcag	cctgggtgac	agagcaagac	tccatctcaa	aacaaaaaca	6780

096,004 - SeqList.ST25.txt

aaaaaaagaa	gattaaaaatt	gtaatttttta	tgtaccgtat	aaatatatac	tctactatat	6840
tagaagttaa	aaattaaaaac	aattataaaaa	ggtaattaac	cacttaaatct	aaaataagaa	6900
caatgtatgt	ggggtttcta	gcttctgaag	aagtaaaagt	tatggccacg	atggcagaaa	6960
tgtgaggagg	gaacagtgga	agttactgtt	gtagacgct	catactctct	gtaagtgact	7020
taatttttaac	caaagacagg	ctggggagaag	ttaaagaggc	attctataag	ccctaaaaca	7080
actgctaata	atggtgaaaag	gtaatctcta	ttaattacca	ataattacag	atatctctaa	7140
aatcgagctg	cagaattggc	acgtctgac	acaccgtcct	ctcattcacg	gtgctttttt	7200
tcttgtgtgc	ttggagattt	tcgattgtgt	gttcgtgttt	ggttaaactt	aatctgtatg	7260
aatcctgaaa	cgaaaaaatgg	tggtgatttc	ctccagaaga	attagagtac	ctggcaggaa	7320
gcagggtggct	ctgtggacct	gagccacttc	aatcttcaag	ggctctctggc	caagaccag	7380
gtgcaaggca	gaggcctgat	gacccgagga	caggaaaagct	cggatgggaa	ggggcgatga	7440
gaagcctgcc	tcgttggtga	gcagcgcatg	aagtgccctt	atttacgctt	tgcaaagatt	7500
gctctggata	ccatctggaa	aaggcggcca	gcgggaatgc	aaggagtcag	aagcctcctg	7560
ctcaaaccga	ggccagcagc	tatggcgccc	acccgggctg	gtgccagagg	gagaggagtc	7620
aaggcacctc	gaagtatggc	ttaaactctt	ttttcacctg	aagcagtgac	caaggtgtat	7680
tctgagggaa	gcttgagtta	ggtgccttct	ttaaaacaga	aagtcattga	agcacccttc	7740
tcaaggga	accagacgcc	cgctctgcgg	tcatttacct	ctttcctctc	tccctctctt	7800
gccctcgcgg	tttctgatcg	ggacagagtg	acccccgtgg	agcttctccg	agccccgtgct	7860
gaggaccctc	ttgcaaaggg	ctccacagac	ccccgccctg	gagagaggag	tctgagcctg	7920
gcttaataac	aaactgggat	gtggctgggg	gcggacagcg	acggcgggat	tcaaagactt	7980
aattccatga	gtaaattcaa	cctttccaca	tccgaatgga	tttggaattt	atcttaatat	8040
tttcttaaat	ttcatcaaat	aacattcagg	agtgcagaaa	tccaaaggcg	taaaacagga	8100
actgagctat	gtttgccaag	gtccaaggac	ttaataacca	tgttcagagg	gatttttcgc	8160
cctaagtact	ttttattggg	tttcataagg	tggcttaggg	tgcaagggaa	agtacacgag	8220
gagaggactg	ggcggcaggg	ctatgagcac	ggcaaggcca	ccggggagag	agtccccggc	8280
ctgggaggct	gacagcagga	ccactgaccg	tcctccctgg	gagctgccac	attgggcaac	8340
gcgaaggcgg	ccacgctgcg	tgtgactcag	gaccccatat	cggcttcctg	ggcccaccca	8400
cactaaccga	ggaagtcacg	gagctctgaa	cccgtggaaa	cgaacatgac	ccttgccctgc	8460
ctgcttcctt	gggtgggtca	agggtaatga	agtgggtgtc	aggaaatggc	catgtaaatt	8520
acacgactct	gctgatgggg	accgttcctt	ccatcattat	tcattctcac	ccccaaggac	8580
tgaatgattc	cagcaacttc	ttcgggtgtg	acaagccatg	acaacactca	gtacaaacac	8640

096,004 - SeqList.ST25.txt

cactctttta	ctaggccac	agagcacggc	ccacaccct	gatatattaa	gagtccagga	8700
gagatgaggc	tgctttcagc	caccaggctg	gggtgacaac	agcggctgaa	cagtctgttc	8760
ctctagacta	gtagaccctg	gcaggcactc	ccccagattc	tagggcctgg	ttgctgcttc	8820
ccgagggcgc	catctgccct	ggagactcag	cctgggggtgc	cacactgagg	ccagccctgt	8880
ctccacaccc	tccgcctcca	ggcctcagct	tctccagcag	cttcctaaac	cctgggtggg	8940
ccgtgttcca	gcgctactgt	ctcacctgtc	ccactgtgtc	ttgtctcagc	gacgtagctc	9000
gcacggttcc	tcctcacatg	gggtgtctgt	ctccttcccc	aacactcaca	tgcgttgaag	9060
ggaggagatt	ctgcgcctcc	cagactggct	cctctgagcc	tgaacctggc	tcgtggcccc	9120
cgatgcaggt	tcctggcgtc	cggctgcacg	ctgacctcca	tttccaggcg	ctccccgtct	9180
cctgtcatct	gccggggcct	gccggtgtgt	tcttctgttt	ctgtgctcct	ttccacgtcc	9240
agctgcgtgt	gtctctgtcc	gctagggtct	cggggttttt	ataggcatag	gacgggggcg	9300
tggtgggcca	gggcgctctt	gggaaatgca	acatttgggt	gtgaaagtag	gagtgcctgt	9360
cctcacctag	gtccacgggc	acaggcctgg	ggatggagcc	cccgccaggg	acccgccctt	9420
ctctgcccag	cacttttctg	ccccctccc	tctggaacac	agagtggcag	tttccacaag	9480
cactaagcat	cctcttccca	aaagacccag	cattggcacc	cctggacatt	tgccccacag	9540
ccctgggaat	tcacgtgact	acgcacatca	tgtacacact	cccgtccacg	accgaccccc	9600
gctgttttat	tttaatagct	acaaagcagg	gaaatccctg	ctaaaatgtc	ctttaacaaa	9660
ctgggttaaac	aaacgggtcc	atccgcacgg	tggacagttc	ctcacagtga	agaggaacat	9720
gccgtttata	aagcctgcag	gcatctcaag	ggaattacgc	tgagtcaaaa	ctgccacctc	9780
catggggatac	gtacgcaaca	tgctcaaaaa	gaaagaattt	caccccatgg	cagggggagtg	9840
gttgggggggt	taaggacgggt	gggggcagca	gctggggggct	actgcacgca	ccttttacta	9900
aagccagttt	cctggttctg	atggtattgg	ctcagttatg	ggagactaac	cataggggag	9960
tggggatggg	ggaacccgga	ggctgtgccca	tctttgccat	gcccagagtgt	cctgggcagg	10020
ataatgctct	agagatgccc	acgtcctgat	tccccaaaac	ctgtggacag	aacccgcccc	10080
gccccagggc	ctttgcagggt	gtgatctccg	tgaggaccct	gaggtctggg	atccttcggg	10140
actacctgca	ggcccgaaaa	gtaatccagg	ggttctggga	agaggcgggc	aggaggggtca	10200
gaggggggca	gcctcaggac	gatggaggca	gtcagtctga	ggctgaaaag	ggagggaggg	10260
cctcgagccc	aggcctgcaa	gcgcctccag	aagctggaaa	aagcggggaa	gggaccctcc	10320
acggagcctg	cagcaggaag	gcacggctgg	cccttagccc	accagggccc	atcgtggacc	10380
tccggcctcc	gtgccatagg	agggcactcg	cgctgccctt	ctagcatgaa	gtgtgtgggg	10440
atttgagaaa	gcaacaggaa	acccatgcac	tgtgaatcta	ggattatttc	aaaacaaagg	10500
tttacagaaa	catccaagga	cagggtgtaa	gtgcctccgg	gcaagggcag	ggcaggcacg	10560

096,004 - SeqList.ST25.txt

agtgatttta	tttagctatt	ttattttatt	tacttacttt	ctgagacaga	gttatgctct	10620
tgttgcccag	gctggagtg	agcggcatga	tcttggctca	ctgcaacctc	cgtctcctgg	10680
gttcaagcaa	ttctcgtgcc	tcagcctccc	aagtagctgg	gatttcaggc	gtgcaccacc	10740
acacccggct	aattttgtat	ttttagtaga	gatgggcttt	caccatgttg	gtcaggctga	10800
tctcaaaatc	ctgacctcag	gtgatccgcc	cacctcagcc	tcccaaagt	ctgggattac	10860
aggcatgagc	cactgcacct	ggcctattta	accattttta	aacttccctg	ggctcaagtc	10920
acacccactg	gtaaggagtt	catggagttc	aatttcccct	ttactcagga	gttaccctcc	10980
tttgatattt	tctgtaattc	ttcgtagact	ggggatacac	cgtctcttga	catattcaca	11040
gtttctgtga	ccacctgtta	tcccatggga	cccactgcag	gggcagctgg	gaggctgcag	11100
gcttcaggtc	ccagtggggt	tgccatctgc	cagtagaaac	ctgatgtaga	atcagggcgc	11160
gagtgtggac	actgtcctga	atctcaatgt	ctcagtgtgt	gctgaaacat	gtagaaatta	11220
aagtccatcc	ctcctactct	actgggattg	agcccccttc	ctatcccccc	ccaggggag	11280
aggagtccct	ctcactcctg	tggaggaagg	aatgatactt	tgttattttt	cactgctggt	11340
actgaatcca	ctgtttcatt	tggttggttg	tttggtttgt	tttgagaggc	ggtttcactc	11400
ttgttgctca	ggctggaggg	agtgcaatgg	cgcgatcttg	gcttactgca	gcctctgcct	11460
cccaggttca	agtgattctc	ctgcttccgc	ctccatttg	gctgggatta	caggcacccg	11520
ccaccatgcc	cagctaattt	tttgatattt	tagtagagac	gggggtgggg	gtgggggttca	11580
ccatgttggc	caggctggtc	tcgaacttct	gacctcagat	gatccacctg	cctctgcctc	11640
ctaaagtgct	gggattacag	gtgtgagcca	ccatgcccag	ctcagaattt	actctgttta	11700
gaaacatctg	ggcttgaggt	aggaagctca	ccccactcaa	gtgttggtgt	gttttaagcc	11760
aatgatagaa	tttttttatt	gttgtagaaa	cactcttgat	gttttacact	gtgatgacta	11820
agacatcatc	agcttttcaa	agacacacta	actgcaccca	taatactggg	gtgtcttctg	11880
ggatcagcg	atcttcattg	aatgccggga	ggcgtttcct	cgccatgcac	atgggtgttaa	11940
ttactccagc	ataatcttct	gcttccattt	cttctcttcc	ctcttttaaa	attgtgtttt	12000
ctatgttggc	ttctctgcag	agaaccagtg	taagctacaa	cttaactttt	gttggaacaa	12060
attttccaaa	ccgccccctt	gccctagtg	cagagacaat	tcacaaacac	agccccctta	12120
aaaggcttag	ggatcactaa	ggggatttct	agaagagcga	cccgtaatcc	taagtattta	12180
caagacgagg	ctaacctcca	gcgagcgtga	cagcccagg	aggggtgcgag	gcctgttcaa	12240
atgctagctc	cataaataaa	gcaatttcct	ccggcagttt	ctgaaagtag	gaaagggttac	12300
atttaagggt	gcgtttgtta	gcatttcagt	gtttgccgac	ctcagctaca	gcatccctgc	12360
aaggcctcgg	gagacccaga	agtttctcgc	cccttagatc	caaacttgag	caacccggag	12420

096,004 - SeqList.ST25.txt

tctggattcc	tgggaagtcc	tcagctgtcc	tgcggtgtg	ccggggcccc	aggtctggag	12480
gggaccagt	gccgtgtggc	ttctactgct	gggctggaag	tcgggcctcc	tagctctgca	12540
gtccgaggct	tggagccagg	tgcctggacc	ccgaggctgc	cctccaccct	gtgcggggcg	12600
gatgtgacca	gatgttggcc	tcactctgcca	gacagagtgc	cggggcccag	ggtcaaggcc	12660
gttggtggctg	gtgtgaggcg	cccggtgcg	ggccagcagg	agcgccctggc	tccatttccc	12720
accctttctc	gacgggaccg	ccccggtggg	tgattaacag	atttggggtg	gtttgctcat	12780
ggtggggacc	cctcgccgcc	tgagaacctg	caaagagaaa	tgacgggcct	gtgtcaagga	12840
gcccgaagt	cggggaagt	ttgcagggag	gactccggg	aggtcccgcg	tgcccgtcca	12900
gggagcaat	cgctctcggg	ttcgtcccca	gccgcgtcta	cgcgccctcg	tcctccccct	12960
cacgtccggc	attcgtggtg	cccggagccc	gacgccccgc	gtccggacct	ggaggcagcc	13020
ctgggtctcc	ggatcaggcc	agcggccaaa	gggtcgccgc	acgcacctgt	tcccaggggc	13080
tccacatcat	ggccccctcc	tcgggttacc	ccacagccta	ggccgattcg	acctctctcc	13140
gctggggccc	tcgctggcgt	ccctgcaccc	tgggagcgcg	agcggcgcg	gggcggggaa	13200
gcgcggccca	gacccccggg	tccgcccggg	gcagctgcgc	tgtcggggcc	aggccgggct	13260
cccagtggat	tcgcgggcac	agacgcccag	gaccgcgctt	cccacgtggc	ggagggactg	13320
gggacccggg	cacccgtcct	gccccctcac	cttccagctc	cgctcctcc	gcgcggaccc	13380
cgccccgtcc	cgacccctcc	cggttccccg	gcccagcccc	ctccggggcc	tcccagcccc	13440
tccccttcct	ttccgcggcc	ccgcccctc	ctcgcggcg	gagtttcagg	cagcgctgcg	13500
tcctgctgcg	cacgtgggaa	gccctggccc	cggccacccc	cgcatgccg	cgcgctcccc	13560
gctgccgagc	cgtgcgtctc	ctgctgcgca	gccactaccg	cgaggtgctg	ccgctggcca	13620
cgttcgtgcg	gcgcctgggg	ccccagggct	ggcggctggt	gcagcgggg	gacccggcg	13680
ctttccgcgc	gctggtggcc	cagtgcctgg	tgtgcgtgcc	ctgggacgca	cggccgcccc	13740
ccgcccggcc	ctccttcgc	cagggtggcc	tccccggggt	cggcgtccgg	ctgggggtga	13800
gggcggccgg	ggggaaccag	cgacatgcgg	agagcagcg	aggcgactca	gggcgcttcc	13860
cccgaggtg	tcctgcctga	aggagctggt	ggcccagagt	ctgcagaggc	tgtgcgagcg	13920
cggcggaag	aacgtgctgg	ccttcggctt	cgcgctgctg	gacggggccc	gcggggggccc	13980
ccccgaggcc	ttcaccacca	gcgtgcgcag	ctacctgccc	aacacgggtga	ccgacgcact	14040
gcgggggagc	ggggcggtgg	ggctgctgct	gcgccgcgtg	ggcgacgacg	tgctggttca	14100
cctgctggca	cgctgcgcgc	tctttgtgct	ggtggctccc	agctgcgcct	accaggtgtg	14160
cgggcccgcg	ctgtaccagc	tcggcgctgc	cactcaggcc	cggccccgc	cacacgctag	14220
tggaccccga	aggcgtctgg	gatgcgaacg	ggcctggaac	catagcgtca	gggaggccgg	14280
ggtccccctg	ggcctgccag	ccccgggtgc	gaggaggcgc	gggggcagtg	ccagccgaag	14340

096,004 - SeqList.ST25.txt

tctgccgttg	cccaagaggc	ccaggcgtgg	cgctgcccct	gagccggagc	ggacgcccgt	14400
tgggcagggg	tcctgggccc	acccgggcag	gacgcgtgga	ccgagtgacc	gtggtttctg	14460
tgtggtgtca	cctgccagac	ccgccgaaga	agccacctct	ttggaggggtg	cgctctcttg	14520
cacgcgccac	tcccacccat	ccgtggggccg	ccagcaccac	gcgggcccc	catccacatc	14580
gcggccacca	cgctccctggg	acacgccttg	tcccccggtg	tacgccgaga	ccaagcactt	14640
cctctactcc	tcaggcgaca	aggagcagct	gcggccctcc	ttcctactca	gctctctgag	14700
gcccagcctg	actggcgctc	ggaggctcgt	ggagaccatc	tttctggggt	ccaggccctg	14760
gatgccaggg	actccccgca	ggttgccccg	cctgccccag	cgctactggc	aaatgcggcc	14820
cctgtttctg	gagctgcttg	ggaaccacgc	gcagtgcccc	tacgggggtgc	tcctcaagac	14880
gactgccccg	ctgcgagctg	cggtcacccc	agcagccggt	gtctgtgccc	gggagaagcc	14940
ccagggctct	gtggcgggccc	ccgaggagga	ggacacagac	ccccgtcgcc	tggtgcagct	15000
gctccgccag	cacagcagcc	cctggcaggt	gtacggcttc	gtgcgggcct	gcctgcgccg	15060
gctggtgccc	ccaggcctct	ggggctccag	gcacaacgaa	cgccgcttcc	tcaggaacac	15120
caagaagttc	atctccctgg	ggaagcatgc	caagctctcg	ctgcaggagc	tgacgtggaa	15180
gatgagcgtg	cgggactgcg	cttggtgctg	caggagccca	ggtgaggagg	tggtggccgt	15240
cgagggccca	ggccccagag	ctgaatgcag	taggggctca	gaaaaggggg	caggcagagc	15300
cctggtcctc	ctgtctccat	cgtcacgtgg	gcacacgtgg	cttttcgctc	aggacgtcga	15360
gtggacacgg	tgatcgagtc	gactcccttt	agtgaggggt	aattgagctc	gcggccgc	15418

<210> 2
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <223> Amplification Primer

<400> 2	
cttgctgcag	aagtgggtgg aggaa
	25

<210> 3
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> Amplification PRimer

<400> 3	
ctgcagtgtg	ggtttcgggc a
	21

<210> 4

<211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> Amplification Primer

<400> 4
 cggaagagtg tctggagcaa 20

<210> 5
 <211> 19
 <212> DNA
 <213> Artificial

<220>
 <223> Amplification Primer

<400> 5
 ggatgaagcg gagtctgga 19

<210> 6
 <211> 1303
 <212> DNA
 <213> Ovis aries

<220>
 <221> CDS
 <222> (194)..(1303)
 <223>

<400> 6
 agccgaggac gccgccgggg agccgaggct ccggccagcc cccagcgcg cccagcttctg 60

cagatcagga gtcagaacgc tgcaccttcg cttcctccca gccctgcctc cttctgcaaa 120

acggagctca atagaacttg gtacttttgc cttttactct gggaggagag aagcagacga 180

tgaggagaaa ata atg aat gtc aaa gga aaa gtg att ctg tca atg ctg 229
 Met Asn Val Lys Gly Lys Val Ile Leu Ser Met Leu
 1 5 10

gtt gtc tca act gtc att gtt gtg ttt tgg gaa tat atc cac agc cca 277
 Val Val Ser Thr Val Ile Val Val Phe Trp Glu Tyr Ile His Ser Pro
 15 20 25

gaa ggc tct ttg ttc tgg ata aac cca tca aga aac cca gaa gtc agt 325
 Glu Gly Ser Leu Phe Trp Ile Asn Pro Ser Arg Asn Pro Glu Val Ser
 30 35 40

ggc ggc agc agc att cag aag ggc tgg tgg ttt ccg aga tgg ttt aac 373
 Gly Gly Ser Ser Ile Gln Lys Gly Trp Trp Phe Pro Arg Trp Phe Asn
 45 50 55 60

aat ggt tac caa gaa gaa gat gaa gac gta gac gaa gaa aag gaa caa 421
 Asn Gly Tyr Gln Glu Glu Asp Glu Asp Val Asp Glu Glu Lys Glu Gln
 65 70 75

aga aag gaa gac aaa agc aag ctt aag cta tcg gac tgg ttc aac cca 469
 Arg Lys Glu Asp Lys Ser Lys Leu Lys Leu Ser Asp Trp Phe Asn Pro
 80 85 90

096,004 - SeqList.ST25.txt

ttt	aaa	cgc	cct	gag	gtt	gtg	act	atg	aca	gat	tgg	aag	gca	ccc	gtg	517
Phe	Lys	Arg	Pro	Glu	Val	Val	Thr	Met	Thr	Asp	Trp	Lys	Ala	Pro	Val	
		95					100					105				
gtg	tgg	gaa	ggc	act	tac	aac	aga	gcc	gtc	tta	gac	gat	tac	tac	gcc	565
Val	Trp	Glu	Gly	Thr	Tyr	Asn	Arg	Ala	Val	Leu	Asp	Asp	Tyr	Tyr	Ala	
	110					115					120					
aag	cag	aaa	att	acc	gtc	ggc	ctg	acg	ggt	ttc	gcc	gtc	gga	aga	tac	613
Lys	Gln	Lys	Ile	Thr	Val	Gly	Leu	Thr	Val	Phe	Ala	Val	Gly	Arg	Tyr	
125					130					135					140	
att	gag	cat	tac	ttg	gag	gag	ttc	tta	acg	tct	gct	aat	aag	cac	ttc	661
Ile	Glu	His	Tyr	Leu	Glu	Glu	Phe	Leu	Thr	Ser	Ala	Asn	Lys	His	Phe	
				145					150					155		
atg	gtt	ggc	cac	cga	gtc	atc	ttt	tac	gtc	atg	gtg	gac	gac	gtc	tcc	709
Met	Val	Gly	His	Arg	Val	Ile	Phe	Tyr	Val	Met	Val	Asp	Asp	Val	Ser	
			160					165					170			
agg	atg	cct	ttg	ata	gag	ctg	ggc	cct	ctg	cgc	tcc	ttc	aaa	gtg	ttt	757
Arg	Met	Pro	Leu	Ile	Glu	Leu	Gly	Pro	Leu	Arg	Ser	Phe	Lys	Val	Phe	
		175					180					185				
gag	gtc	aag	cct	gag	agg	agg	tgg	cag	gac	gtc	agc	atg	gtg	cgc	atg	805
Glu	Val	Lys	Pro	Glu	Arg	Arg	Trp	Gln	Asp	Val	Ser	Met	Val	Arg	Met	
	190					195					200					
aag	acc	atc	ggg	gag	cac	atc	gtg	gcc	cac	atc	cag	cgt	gag	gtt	gac	853
Lys	Thr	Ile	Gly	Glu	His	Ile	Val	Ala	His	Ile	Gln	Arg	Glu	Val	Asp	
205					210					215					220	
ttc	ctc	ttc	tgc	atg	gac	gtg	gac	cag	gtc	ttc	caa	gac	gag	ttc	ggg	901
Phe	Leu	Phe	Cys	Met	Asp	Val	Asp	Gln	Val	Phe	Gln	Asp	Glu	Phe	Gly	
				225					230					235		
gtg	gag	acc	ctg	ggt	gag	tcg	gtg	gcc	cag	cta	cag	gcc	tgg	tgg	tac	949
Val	Glu	Thr	Leu	Gly	Glu	Ser	Val	Ala	Gln	Leu	Gln	Ala	Trp	Trp	Tyr	
			240					245					250			
aag	gca	gat	ccc	gat	gag	ttt	acc	tac	gag	agg	cgc	aag	gag	tct	gca	997
Lys	Ala	Asp	Pro	Asp	Glu	Phe	Thr	Tyr	Glu	Arg	Arg	Lys	Glu	Ser	Ala	
		255					260					265				
gca	tac	att	ccc	ttc	ggc	gaa	ggg	gat	ttt	tat	tac	cac	gca	gcc	att	1045
Ala	Tyr	Ile	Pro	Phe	Gly	Glu	Gly	Asp	Phe	Tyr	Tyr	His	Ala	Ala	Ile	
	270					275					280					
ttt	ggg	gga	aca	ccc	act	cag	gtc	ctt	aac	atc	acc	cag	gaa	tgc	ttc	1093
Phe	Gly	Gly	Thr	Pro	Thr	Gln	Val	Leu	Asn	Ile	Thr	Gln	Glu	Cys	Phe	
285					290					295					300	
aaa	gga	atc	ctc	aag	gac	aag	aaa	aat	gac	ata	gaa	gcc	caa	tgg	cat	1141
Lys	Gly	Ile	Leu	Lys	Asp	Lys	Lys	Asn	Asp	Ile	Glu	Ala	Gln	Trp	His	
				305					310					315		
gat	gag	agc	cat	cta	aac	aag	tat	ttc	ctt	ctc	aac	aaa	ccc	act	aaa	1189
Asp	Glu	Ser	His	Leu	Asn	Lys	Tyr	Phe	Leu	Leu	Asn	Lys	Pro	Thr	Lys	
			320					325					330			
atc	tta	tcc	ccg	gaa	tac	tgc	tgg	gat	tat	cat	ata	ggc	cta	cct	gcg	1237
Ile	Leu	Ser	Pro	Glu	Tyr	Cys	Trp	Asp	Tyr	His	Ile	Gly	Leu	Pro	Ala	

335

gat att aag ctt gtc aag atg tct tgg cag aca aaa gag tat aat gtg 1285
Asp Ile Lys Leu Val Lys Met Ser Trp Gln Thr Lys Glu Tyr Asn Val
350 355 360

gtt aga aat aac gtc tga 1303
Val Arg Asn Asn Val
365

<210> 7
<211> 369
<212> PRT
<213> Ovis aries

<400> 7

Met Asn Val Lys Gly Lys Val Ile Leu Ser Met Leu Val Val Ser Thr
1 5 10 15

Val Ile Val Val Phe Trp Glu Tyr Ile His Ser Pro Glu Gly Ser Leu
20 25 30

Phe Trp Ile Asn Pro Ser Arg Asn Pro Glu Val Ser Gly Gly Ser Ser
35 40 45

Ile Gln Lys Gly Trp Trp Phe Pro Arg Trp Phe Asn Asn Gly Tyr Gln
50 55 60

Glu Glu Asp Glu Asp Val Asp Glu Glu Lys Glu Gln Arg Lys Glu Asp
65 70 75 80

Lys Ser Lys Leu Lys Leu Ser Asp Trp Phe Asn Pro Phe Lys Arg Pro
85 90 95

Glu Val Val Thr Met Thr Asp Trp Lys Ala Pro Val Val Trp Glu Gly
100 105 110

Thr Tyr Asn Arg Ala Val Leu Asp Asp Tyr Tyr Ala Lys Gln Lys Ile
115 120 125

Thr Val Gly Leu Thr Val Phe Ala Val Gly Arg Tyr Ile Glu His Tyr
130 135 140

Leu Glu Glu Phe Leu Thr Ser Ala Asn Lys His Phe Met Val Gly His
145 150 155 160

Arg Val Ile Phe Tyr Val Met Val Asp Asp Val Ser Arg Met Pro Leu
165 170 175

Ile Glu Leu Gly Pro Leu Arg Ser Phe Lys Val Phe Glu Val Lys Pro
Page 12

180

Glu Arg Arg Trp Gln Asp Val Ser Met Val Arg Met Lys Thr Ile Gly
195 200 205
Glu His Ile Val Ala His Ile Gln Arg Glu Val Asp Phe Leu Phe Cys
210 215 220
Met Asp Val Asp Gln Val Phe Gln Asp Glu Phe Gly Val Glu Thr Leu
225 230 235 240
Gly Glu Ser Val Ala Gln Leu Gln Ala Trp Trp Tyr Lys Ala Asp Pro
245 250 255
Asp Glu Phe Thr Tyr Glu Arg Arg Lys Glu Ser Ala Ala Tyr Ile Pro
260 265 270
Phe Gly Glu Gly Asp Phe Tyr Tyr His Ala Ala Ile Phe Gly Gly Thr
275 280 285
Pro Thr Gln Val Leu Asn Ile Thr Gln Glu Cys Phe Lys Gly Ile Leu
290 295 300
Lys Asp Lys Lys Asn Asp Ile Glu Ala Gln Trp His Asp Glu Ser His
305 310 315 320
Leu Asn Lys Tyr Phe Leu Leu Asn Lys Pro Thr Lys Ile Leu Ser Pro
325 330 335
Glu Tyr Cys Trp Asp Tyr His Ile Gly Leu Pro Ala Asp Ile Lys Leu
340 345 350
Val Lys Met Ser Trp Gln Thr Lys Glu Tyr Asn Val Val Arg Asn Asn
355 360 365

Val

<210> 8
<211> 1131
<212> DNA
<213> Platyrrhinus helleri

<220>
<221> CDS
<222> (1)..(1131)
<223>

<400> 8
atg aat gtc aaa gga aaa gta att ctg tcg atg ctg gtt gtc tca act
Page 13

096,004 - SeqList.ST25.txt

Met 1	Asn	Val	Lys	Gly 5	Lys	Val	Ile	Leu	Ser 10	Met	Leu	Val	Val	Ser 15	Thr		
gtg Val	att Ile	gtt Val	gtg Val 20	ttt Phe	tgg Trp	gaa Glu	tat Tyr	atc Ile 25	aac Asn	agc Ser	cca Pro	gaa Glu	ggc Gly 30	tct Ser	ttc Phe		96
ttg Leu	tgg Trp	ata Ile 35	tat Tyr	cac His	tca Ser	aag Lys	aac Asn 40	cca Pro	gaa Glu	gtt Val	gat Asp	gac Asp 45	agc Ser	agt Ser	gct Ala		144
cag Gln	aag Lys 50	gac Asp	tgg Trp	tgg Trp	ttt Phe	cct Pro 55	ggc Gly	tgg Trp	ttt Phe	aac Asn	aat Asn 60	ggg Gly	atc Ile	cac His	aat Asn		192
tat Tyr 65	caa Gln	caa Gln	gag Glu	gaa Glu	gaa Glu 70	gac Asp	aca Thr	gac Asp	aaa Lys	gaa Glu 75	aaa Lys	gga Gly	aga Arg	gag Glu	gag Glu 80		240
gaa Glu	caa Gln	aaa Lys	aag Lys	gaa Glu 85	gat Asp	gac Asp	aca Thr	aca Thr	gag Glu 90	ctt Leu	cgg Arg	cta Leu	tgg Trp	gac Asp 95	tgg Trp		288
ttt Phe	aat Asn	cca Pro	aag Lys 100	aaa Lys	cgc Arg	cca Pro	gag Glu	gtt Val 105	atg Met	aca Thr	gtg Val	acc Thr	caa Gln 110	tgg Trp	aag Lys		336
gcg Ala	ccg Pro	gtt Val 115	gtg Val	tgg Trp	gaa Glu	ggc Gly	act Thr 120	tac Tyr	aac Asn	aaa Lys	gcc Ala	atc Ile 125	cta Leu	gaa Glu	aat Asn		384
tat Tyr	tat Tyr 130	gcc Ala	aaa Lys	cag Gln	aaa Lys	att Ile 135	acc Thr	gtg Val	ggg Gly	ttg Leu	acg Thr 140	gtt Val	ttt Phe	gct Ala	att Ile		432
gga Gly 145	aga Arg	tat Tyr	att Ile	gag Glu	cat His 150	tac Tyr	ttg Leu	gag Glu	gag Glu 155	ttc Phe	gta Val	aca Thr	tct Ser	gct Ala	aat Asn 160		480
agg Arg	tac Tyr	ttc Phe	atg Met	gtc Val 165	ggc Gly	cac His	aaa Lys	gtc Val 170	ata Ile 170	ttt Phe	tat Tyr	gtc Val	atg Met	gtg Val 175	gat Asp		528
gat Asp	gtc Val	tcc Ser	aag Lys 180	gcg Ala	ccg Pro	ttt Phe	ata Ile	gag Glu 185	ctg Leu	ggt Gly	cct Pro	ctg Leu	cgt Arg 190	tcc Ser	ttc Phe		576
aaa Lys	gtg Val	ttt Phe 195	gag Glu	gtc Val	aag Lys	cca Pro	gag Glu 200	aag Lys	agg Arg	tgg Trp	caa Gln	gac Asp 205	atc Ile	agc Ser	atg Met		624
atg Met 210	cgt Arg	atg Met	aag Lys	acc Thr	atc Ile	ggg Gly 215	gag Glu	cac His	atc Ile	ttg Leu	gcc Ala 220	cac His	atc Ile	caa Gln	cac His		672
gag Glu 225	gtt Val	gac Asp	ttc Phe	ctc Leu	ttc Phe 230	tgc Cys	atg Met	gat Asp	gtg Val	gac Asp 235	cag Gln	gtc Val	ttc Phe	caa Gln	gac Asp 240		720
cat His	ttt Phe	ggg Gly	gta Val	gag Glu 245	acc Thr	ctg Leu	ggc Gly	cag Gln	tcg Ser 250	gtg Val	gct Ala	cag Gln	cta Leu	cag Gln 255	gcc Ala		768

096,004 - SeqList.ST25.txt

tgg tgg tac aag gca gat cct gat gac ttt acc tat gag agg cgg aaa	816
Trp Trp Tyr Lys Ala Asp Pro Asp Asp Phe Thr Tyr Glu Arg Arg Lys	
260 265 270	
gag tcg gca gca tat att cca ttt ggc cag ggg gat ttt tat tac cat	864
Glu Ser Ala Ala Tyr Ile Pro Phe Gly Gln Gly Asp Phe Tyr Tyr His	
275 280 285	
gca gcc att ttt gga gga aca ccg att cag gtt ctc aac atc acc cag	912
Ala Ala Ile Phe Gly Gly Thr Pro Ile Gln Val Leu Asn Ile Thr Gln	
290 295 300	
gag tgc ttt aag gga atc ctc ctg gac aag aaa aat gac ata gaa gcc	960
Glu Cys Phe Lys Gly Ile Leu Leu Asp Lys Lys Asn Asp Ile Glu Ala	
305 310 315 320	
gag tgg cat gat gaa agc cac cta aac aag tat ttc ctt ctc aac aaa	1008
Glu Trp His Asp Glu Ser His Leu Asn Lys Tyr Phe Leu Leu Asn Lys	
325 330 335	
ccc tct aaa atc tta tct cca gaa tac tgc tgg gat tat cat ata ggc	1056
Pro Ser Lys Ile Leu Ser Pro Glu Tyr Cys Trp Asp Tyr His Ile Gly	
340 345 350	
ctg cct tca gat att aaa act gtc aag cta tca tgg caa aca aaa gag	1104
Leu Pro Ser Asp Ile Lys Thr Val Lys Leu Ser Trp Gln Thr Lys Glu	
355 360 365	
tat aat ttg gtt aga aag aat gtc tga	1131
Tyr Asn Leu Val Arg Lys Asn Val	
370 375	

<210> 9
 <211> 376
 <212> PRT
 <213> *Platyrrhinus helleri*

<400> 9

Met Asn Val Lys Gly Lys Val Ile Leu Ser Met Leu Val Val Ser Thr
1 5 10 15
Val Ile Val Val Phe Trp Glu Tyr Ile Asn Ser Pro Glu Gly Ser Phe
20 25 30
Leu Trp Ile Tyr His Ser Lys Asn Pro Glu Val Asp Asp Ser Ser Ala
35 40 45
Gln Lys Asp Trp Trp Phe Pro Gly Trp Phe Asn Asn Gly Ile His Asn
50 55 60
Tyr Gln Gln Glu Glu Glu Asp Thr Asp Lys Glu Lys Gly Arg Glu Glu
65 70 75 80
Glu Gln Lys Lys Glu Asp Asp Thr Thr Glu Leu Arg Leu Trp Asp Trp
85 90 95

096,004 - SeqList.ST25.txt

Phe Asn Pro Lys Lys Arg Pro Glu Val Met Thr Val Thr Gln Trp Lys
100 105 110

Ala Pro Val Val Trp Glu Gly Thr Tyr Asn Lys Ala Ile Leu Glu Asn
115 125

Tyr Tyr Ala Lys Gln Lys Ile Thr Val Gly Leu Thr Val Phe Ala Ile
130 135 140

Gly Arg Tyr Ile Glu His Tyr Leu Glu Glu Phe Val Thr Ser Ala Asn
145 150 155 160

Arg Tyr Phe Met Val Gly His Lys Val Ile Phe Tyr Val Met Val Asp
165 170 175

Asp Val Ser Lys Ala Pro Phe Ile Glu Leu Gly Pro Leu Arg Ser Phe
180 185 190

Lys Val Phe Glu Val Lys Pro Glu Lys Arg Trp Gln Asp Ile Ser Met
195 200 205

Met Arg Met Lys Thr Ile Gly Glu His Ile Leu Ala His Ile Gln His
210 215 220

Glu Val Asp Phe Leu Phe Cys Met Asp Val Asp Gln Val Phe Gln Asp
225 230 235 240

His Phe Gly Val Glu Thr Leu Gly Gln Ser Val Ala Gln Leu Gln Ala
245 250 255

Trp Trp Tyr Lys Ala Asp Pro Asp Asp Phe Thr Tyr Glu Arg Arg Lys
260 265 270

Glu Ser Ala Ala Tyr Ile Pro Phe Gly Gln Gly Asp Phe Tyr Tyr His
275 280 285

Ala Ala Ile Phe Gly Gly Thr Pro Ile Gln Val Leu Asn Ile Thr Gln
290 295 300

Glu Cys Phe Lys Gly Ile Leu Leu Asp Lys Lys Asn Asp Ile Glu Ala
305 310 315 320

Glu Trp His Asp Glu Ser His Leu Asn Lys Tyr Phe Leu Leu Asn Lys
325 330 335

Pro Ser Lys Ile Leu Ser Pro Glu Tyr Cys Trp Asp Tyr His Ile Gly
340 345 350

096,004 - SeqList.ST25.txt

Leu Pro Ser Asp Ile Lys Thr Val Lys Leu Ser Trp Gln Thr Lys Glu
355 360 365

Tyr Asn Leu Val Arg Lys Asn Val
370 375

<210> 10
<211> 1062
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1062)
<223>

<400> 10
atg gcc gag gtg ttg cgg acg ctg gcc gga aaa cca aaa tgc cac gca 48
Met Ala Glu Val Leu Arg Thr Leu Ala Gly Lys Pro Lys Cys His Ala
1 5 10 15
ctt cga cct atg atc ctt ttc cta ata atg ctt gtc ttg gtc ttg ttt 96
Leu Arg Pro Met Ile Leu Phe Leu Ile Met Leu Val Leu Val Leu Phe
20 25 30
ggt tac ggg gtc cta agc ccc aga agt cta atg cca gga agc ctg gaa 144
Gly Tyr Gly Val Leu Ser Pro Arg Ser Leu Met Pro Gly Ser Leu Glu
35 40 45
cgg ggg ttc tgc atg gct gtt agg gaa cct gac cat ctg cag cgc gtc 192
Arg Gly Phe Cys Met Ala Val Arg Glu Pro Asp His Leu Gln Arg Val
50 55 60
tcg ttg cca agg atg gtc tac ccc cag cca aag gtg ctg aca ccg tgg 240
Ser Leu Pro Arg Met Val Tyr Pro Gln Pro Lys Val Leu Thr Pro Trp
65 70 75 80
aag gat gtc ctc gtg gtg acc cct tgg ctg gct ccc att gtc tgg gag 288
Lys Asp Val Leu Val Val Thr Pro Trp Leu Ala Pro Ile Val Trp Glu
85 90 95
ggc aca ttc aac atc gac atc ctc aac gag cag ttc agg ctc cag aac 336
Gly Thr Phe Asn Ile Asp Ile Leu Asn Glu Gln Phe Arg Leu Gln Asn
100 105 110
acc acc att ggg tta act gtg ttt gcc atc aag aaa tac gtg gct ttc 384
Thr Thr Ile Gly Leu Thr Val Phe Ala Ile Lys Lys Tyr Val Ala Phe
115 120 125
ctg aag ctg ttc ctg gag acg gcg gag aag cac ttc atg gtg ggc cac 432
Leu Lys Leu Phe Leu Glu Thr Ala Glu Lys His Phe Met Val Gly His
130 135 140
cgt gtc cac tac tat gtc ttc acc gac cag ctg gcc gcg gtg ccc cgc 480
Arg Val His Tyr Tyr Val Phe Thr Asp Gln Leu Ala Ala Val Pro Arg
145 150 155 160
gtg acg ctg ggg acc ggt cgg cag ctg tca gtg ctg gag gtg cgc gcc 528
Val Thr Leu Gly Thr Gly Arg Gln Leu Ser Val Leu Glu Val Arg Ala

096,004 - SeqList.ST25.txt

165	170	175	
tac aag cgc tgg cag gac gtg tcc atg cgc cgc atg gag atg atc agt Tyr Lys Arg Trp Gln Asp Val Ser Met Arg Arg Met Glu Met Ile Ser 180 185 190			576
gac ttc tgc gag cgg cgc ttc ctc agc gag gtg gat tac ctg gtg tgc Asp Phe Cys Glu Arg Arg Phe Leu Ser Glu Val Asp Tyr 205 195 200			624
gtg gac gtg gac atg gag ttc cgc gac cac gtg ggc gtg gag atc ctg Val Asp Val Asp Met Glu Phe Arg Asp His Val Gly Val Glu Ile Leu 210 215 220			672
act ccg ctg ttc ggc acc ctg cac ccc ggc ttc tac gga agc agc cgg Thr Pro Leu Phe Gly Thr Leu His Pro Gly Phe Tyr Gly Ser Ser Arg 225 230 235 240			720
gag gcc ttc acc tac gag cgc cgg ccc cag tcc cag gcc tac atc ccc Glu Ala Phe Thr Tyr Glu Arg Arg Pro Gln Ser Gln Ala Tyr Ile Pro 245 250 255			768
aag gac gag ggc gat ttc tac tac ctg ggg ggg ttc ttc ggg ggg tcg Lys Asp Glu Gly Asp Phe Tyr Tyr Leu Gly Gly Phe Phe Gly Gly Ser 260 265 270			816
gtg caa gag gtg cag cgg ctc acc agg gcc tgc cac cag gcc atg atg Val Gln Glu Val Gln Arg Leu Thr Arg Ala Cys His Gln Ala Met Met 275 280 285			864
gtc gac cag gcc aac ggc atc gag gcc gtg tgg cac gac gag agc cac Val Asp Gln Ala Asn Gly Ile Glu Ala Val Trp His Asp Glu Ser His 290 295 300			912
ctg aac aag tac ctg ctg cgc cac aaa ccc acc aag gtg ctc tcc ccc Leu Asn Lys Tyr Leu Leu Arg His Lys Pro Thr Lys Val Leu Ser Pro 305 310 315 320			960
gag tac ttg tgg gac cag cag ctg ctg ggc tgg ccc gcc gtc ctg agg Glu Tyr Leu Trp Asp Gln Gln Leu Leu Gly Trp Pro Ala Val Leu Arg 325 330 335			1008
aag ctg agg ttc act gcg gtg ccc aag aac cac cag gcg gtc cgg aac Lys Leu Arg Phe Thr Ala Val Pro Lys Asn His Gln Ala Val Arg Asn 340 345 350			1056
ccg tga Pro			1062

<210> 11
 <211> 353
 <212> PRT
 <213> Homo sapiens

<400> 11

Met Ala Glu Val Leu Arg Thr Leu Ala Gly Lys Pro Lys Cys His Ala
 1 5 10 15

Leu Arg Pro Met Ile Leu Phe Leu Ile Met Leu Val Leu Val Leu Phe
 Page 18

20

25

30

Gly Tyr Gly Val Leu Ser Pro Arg Ser Leu Met Pro Gly Ser Leu Glu
 35 40 45

Arg Gly Phe Cys Met Ala Val Arg Glu Pro Asp His Leu Gln Arg Val
 50 55 60

Ser Leu Pro Arg Met Val Tyr Pro Gln Pro Lys Val Leu Thr Pro Trp
 65 70 75 80

Lys Asp Val Leu Val Val Thr Pro Trp Leu Ala Pro Ile Val Trp Glu
 85 90 95

Gly Thr Phe Asn Ile Asp Ile Leu Asn Glu Gln Phe Arg Leu Gln Asn
 100 105 110

Thr Thr Ile Gly Leu Thr Val Phe Ala Ile Lys Lys Tyr Val Ala Phe
 115 120 125

Leu Lys Leu Phe Leu Glu Thr Ala Glu Lys His Phe Met Val Gly His
 130 135 140

Arg Val His Tyr Tyr Val Phe Thr Asp Gln Leu Ala Ala Val Pro Arg
 145 150 155 160

Val Thr Leu Gly Thr Gly Arg Gln Leu Ser Val Leu Glu Val Arg Ala
 165 170 175

Tyr Lys Arg Trp Gln Asp Val Ser Met Arg Arg Met Glu Met Ile Ser
 180 185 190

Asp Phe Cys Glu Arg Arg Phe Leu Ser Glu Val Asp Tyr Leu Val Cys
 195 200 205

Val Asp Val Asp Met Glu Phe Arg Asp His Val Gly Val Glu Ile Leu
 210 215 220

Thr Pro Leu Phe Gly Thr Leu His Pro Gly Phe Tyr Gly Ser Ser Arg
 225 230 235 240

Glu Ala Phe Thr Tyr Glu Arg Arg Pro Gln Ser Gln Ala Tyr Ile Pro
 245 250 255

Lys Asp Glu Gly Asp Phe Tyr Tyr Leu Gly Gly Phe Phe Gly Gly Ser
 260 265 270

096,004 - SeqList.ST25.txt

Val Gln Glu Val Gln Arg Leu Thr Arg Ala Cys His Gln Ala Met Met
275 280 285

Val Asp Gln Ala Asn Gly Ile Glu Ala Val Trp His Asp Glu Ser His
290 295 300

Leu Asn Lys Tyr Leu Leu Arg His Lys Pro Thr Lys Val Leu Ser Pro
305 310 315 320

Glu Tyr Leu Trp Asp Gln Gln Leu Leu Gly Trp Pro Ala Val Leu Arg
325 330 335

Lys Leu Arg Phe Thr Ala Val Pro Lys Asn His Gln Ala Val Arg Asn
340 345 350

Pro

<210> 12
<211> 1065
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1065)
<223>

<400> 12	
atg gcc gag gtg ttg cgg acg ctg gcc gga aaa cca aaa tgc cac gca	48
Met Ala Glu Val Leu Arg Thr Leu Ala Gly Lys Pro Lys Cys His Ala	
1 5 10 15	
ctt cga cct atg atc ctt ttc cta ata atg ctt gtc ttg gtc ttg ttt	96
Leu Arg Pro Met Ile Leu Phe Leu Ile Met Leu Val Leu Val Leu Phe	
20 25 30	
ggt tac ggg gtc cta agc ccc aga agt cta atg cca gga agc ctg gaa	144
Gly Tyr Gly Val Leu Ser Pro Arg Ser Leu Met Pro Gly Ser Leu Glu	
35 40 45	
cgg ggg ttc tgc atg gct gtt agg gaa cct gac cat ctg cag cgc gtc	192
Arg Gly Phe Cys Met Ala Val Arg Glu Pro Asp His Leu Gln Arg Val	
50 55 60	
tcg ttg cca agg atg gtc tac ccc cag cca aag gtg ctg aca ccg tgt	240
Ser Leu Pro Arg Met Val Tyr Pro Gln Pro Lys Val Leu Thr Pro Cys	
65 70 75 80	
agg aag gat gtc ctc gtg gtg acc cct tgg ctg gct ccc att gtc tgg	288
Arg Lys Asp Val Leu Val Val Thr Pro Trp Leu Ala Pro Ile Val Trp	
85 90 95	
gag ggc acg ttc aac atc gac atc ctc aac gag cag ttc agg ctc cag	336
Glu Gly Thr Phe Asn Ile Asp Ile Leu Asn Glu Gln Phe Arg Leu Gln	
100 105 110	

096,004 - SeqList.ST25.txt

aac Asn	acc Thr	acc Thr 115	att Ile	ggg Gly	tta Leu	act Thr	gtg Val 120	ttt Phe	gcc Ala	atc Ile	aag Lys	aaa Lys 125	tac Tyr	gtg Val	gct Ala	384
ttc Phe	ctg Leu 130	aag Lys	ctg Leu	ttc Phe	ctg Leu	gag Glu 135	acg Thr	gcg Ala	gag Glu	aag Lys	cac His 140	ttc Phe	atg Met	gtg Val	ggc Gly	432
cac His 145	cgt Arg	gtc Val	cac His	tac Tyr	tat Tyr 150	gtc Val	ttc Phe	acc Thr	gac Asp	cag Gln 155	ccg Pro	gcc Ala	gcg Ala	gtg Val	ccc Pro 160	480
cgc Arg	gtg Val	acg Thr	ctg Leu	ggg Gly 165	acc Thr	ggt Gly	cgg Arg	cag Gln	ctg Leu 170	tca Ser	gtg Val	ctg Leu	gag Glu	gtg Val 175	ggc Gly	528
gcc Ala	tac Tyr	aag Lys	cgc Arg 180	tgg Trp	cag Gln	gac Asp	gtg Val 185	tcc Ser	atg Met	cgc Arg	cgc Arg	atg Met	gag Glu 190	atg Met	atc Ile	576
agt Ser	gac Asp	ttc Phe 195	tgc Cys	gag Glu	cgg Arg	cgc Arg	ttc Phe 200	ctc Leu	agc Ser	gag Glu	gtg Val	gat Asp 205	tac Tyr	ctg Leu	gtg Val	624
tgc Cys	gtg Val 210	gac Asp	gtg Val	gac Asp	atg Met	gag Glu 215	ttc Phe	cgc Arg	gac Asp	cat His	gtg Val 220	ggc Gly	gtg Val	gag Glu	atc Ile	672
ctg Leu 225	act Thr	ccg Pro	ctg Leu	ttc Phe	ggc Gly 230	acc Thr	ctg Leu	cac His	ccc Pro	agc Ser 235	ttc Phe	tac Tyr	gga Gly	agc Ser	agc Ser 240	720
cgg Arg	gag Glu	gcc Ala	ttc Phe	acc Thr 245	tac Tyr	gag Glu	cgc Arg	cgg Arg	ccc Pro 250	cag Gln	tcc Ser	cag Gln	gcc Ala	tac Tyr 255	atc Ile	768
ccc Pro	aag Lys	gac Asp	gag Glu 260	ggc Gly	gat Asp	ttc Phe	tac Tyr	tac Tyr 265	atg Met	ggg Gly	gcg Ala	ttc Phe	ttc Phe 270	ggg Gly	ggg Gly	816
tcg Ser	gtg Val	caa Gln 275	gag Glu	gtg Val	cag Gln	cgg Arg	ctc Leu 280	acc Thr	agg Arg	gcc Ala	tgc Cys	cac His 285	cag Gln	gcc Ala	atg Met	864
atg Met	gtc Val 290	gac Asp	cag Gln	gcc Ala	aac Asn	ggc Gly 295	atc Ile	gag Glu	gcc Ala	gtg Val	tgg Trp 300	cac His	gac Asp	gag Glu	agc Ser	912
cac His 305	ctg Leu	aac Asn	aag Lys	tac Tyr	cta Leu 310	ctg Leu	cgc Arg	cac His	aaa Lys	ccc Pro 315	acc Thr	aag Lys	gtg Val	ctc Leu	tcc Ser 320	960
ccc Pro	gag Glu	tac Tyr	ttg Leu	tgg Trp 325	gac Asp	cag Gln	cag Gln	ctg Leu	ctg Leu 330	ggc Gly	tgg Trp	ccc Pro	gcc Ala	gtc Val 335	ctg Leu	1008
agg Arg	aag Lys	ctg Leu	agg Arg 340	ttc Phe	act Thr	gcg Ala	gtg Val	ccc Pro 345	aag Lys	aac Asn	cac His	cag Gln	gcg Ala 350	gtc Val	cgg Arg	1056
aac Asn	ccg Pro	tga														1065

096,004 - SeqList.ST25.txt

<210> 13
 <211> 354
 <212> PRT
 <213> Homo sapiens

<400> 13

Met Ala Glu Val Leu Arg Thr Leu Ala Gly Lys Pro Lys Cys His Ala
 1 5 10 15

Leu Arg Pro Met Ile Leu Phe Leu Ile Met Leu Val Leu Val Leu Phe
 20 25 30

Gly Tyr Gly Val Leu Ser Pro Arg Ser Leu Met Pro Gly Ser Leu Glu
 35 40 45

Arg Gly Phe Cys Met Ala Val Arg Glu Pro Asp His Leu Gln Arg Val
 50 55 60

Ser Leu Pro Arg Met Val Tyr Pro Gln Pro Lys Val Leu Thr Pro Cys
 65 70 75 80

Arg Lys Asp Val Leu Val Val Thr Pro Trp Leu Ala Pro Ile Val Trp
 85 90 95

Glu Gly Thr Phe Asn Ile Asp Ile Leu Asn Glu Gln Phe Arg Leu Gln
 100 105 110

Asn Thr Thr Ile Gly Leu Thr Val Phe Ala Ile Lys Lys Tyr Val Ala
 115 120 125

Phe Leu Lys Leu Phe Leu Glu Thr Ala Glu Lys His Phe Met Val Gly
 130 135 140

His Arg Val His Tyr Tyr Val Phe Thr Asp Gln Pro Ala Ala Val Pro
 145 150 155 160

Arg Val Thr Leu Gly Thr Gly Arg Gln Leu Ser Val Leu Glu Val Gly
 165 170 175

Ala Tyr Lys Arg Trp Gln Asp Val Ser Met Arg Arg Met Glu Met Ile
 180 185 190

Ser Asp Phe Cys Glu Arg Arg Phe Leu Ser Glu Val Asp Tyr Leu Val
 195 200 205

Cys Val Asp Val Asp Met Glu Phe Arg Asp His Val Gly Val Glu Ile
 210 215 220

096,004 - SeqList.ST25.txt

Leu Thr Pro Leu Phe Gly Thr Leu His Pro Ser Phe Tyr Gly Ser Ser
 225 230 235 240

Arg Glu Ala Phe Thr Tyr Glu Arg Arg Pro Gln Ser Gln Ala Tyr Ile
 245 250 255

Pro Lys Asp Glu Gly Asp Phe Tyr Tyr Met Gly Ala Phe Phe Gly Gly
 260 265 270

Ser Val Gln Glu Val Gln Arg Leu Thr Arg Ala Cys His Gln Ala Met
 275 280 285

Met Val Asp Gln Ala Asn Gly Ile Glu Ala Val Trp His Asp Glu Ser
 290 295 300

His Leu Asn Lys Tyr Leu Leu Arg His Lys Pro Thr Lys Val Leu Ser
 305 310 315 320

Pro Glu Tyr Leu Trp Asp Gln Gln Leu Leu Gly Trp Pro Ala Val Leu
 325 330 335

Arg Lys Leu Arg Phe Thr Ala Val Pro Lys Asn His Gln Ala Val Arg
 340 345 350

Asn Pro

<210> 14
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Amplification Primer

<220>
 <221> misc_feature
 <222> (1)..(23)
 <223> Amplification Primer

<400> 14
 ggcctgtact acatttgcct gga

23

<210> 15
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Amplification Primer

096,004 - SeqList.ST25.txt

<220>
 <221> misc_feature
 <222> (1)..(26)
 <223> Amplification Primer

<400> 15
 gaaatagtgt caagtttcca tcacaa

26

<210> 16
 <211> 55
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Amplification Primer

<220>
 <221> misc_feature
 <222> (1)..(55)
 <223> Amplification Primer

<400> 16
 cgatgtggct gcggagccac cggcaggtaa tcctgttgat gctgattgtc tcaac

55

<210> 17
 <211> 50
 <212> PRT
 <213> Mus musculus

<400> 17

Met Ile Thr Met Leu Gln Asp Leu His Val Asn Lys Ile Ser Met Ser
 1 5 10 15

Arg Ser Lys Ser Glu Thr Ser Leu Pro Ser Ser Arg Ser Gly Ser Gln
 20 25 30

Glu Lys Ile Met Asn Val Lys Gly Lys Val Ile Leu Leu Met Leu Ile
 35 40 45

Val Ser
 50

<210> 18
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chimera Mouse/Pig

<400> 18

Met Trp Leu Arg Ser His Arg Gln Val Ile Leu Leu Met Leu Ile Val
 Page 24

1 5 10 15

Ser

<210> 19
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chimera Mouse/Pig

<400> 19

Met Trp Leu Arg Ser His Arg Gln Val Val Leu Ser Met Leu Leu Val
 1 5 10 15

Ser

<210> 20
 <211> 15
 <212> PRT
 <213> Sus scrofa

<400> 20

Met Asn Val Lys Gly Arg Val Val Leu Ser Met Leu Leu Val Ser
 1 5 10 15